

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/764,131

Source: _____

Date Processed by STIC: _____

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IFWO

RAW SEQUENCE LISTING DATE: 03/09/2005
 PATENT APPLICATION: US/10/764,131 TIME: 09:51:18

Input Set : N:\Crif3\RULE60\10764131.raw.txt
 Output Set: N:\CRF4\03092005\J764131.raw

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1 <110> APPLICANT: KELER, Tibor
2      GOLDSTEIN, Joel
3      GRAZIANO, Robert
4      DEO, Yashwant M.
5 <120> TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR
6      BINDING COMPONENTS
7 <130> FILE REFERENCE: MXI-099CPA
8 <140> CURRENT APPLICATION NUMBER: US/10/764,131
9 <141> CURRENT FILING DATE: 2004-01-23
10 <150> PRIOR APPLICATION NUMBER: US/09/203,958
11 <151> PRIOR FILING DATE: 1998-12-02
12 <150> PRIOR APPLICATION NUMBER: 60/067232
13 <151> PRIOR FILING DATE: 1997-12-02
14 <160> NUMBER OF SEQ ID NOS: 4
15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1132
19 <212> TYPE: DNA
20 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
22 <223> OTHER INFORMATION: Synthetic construct
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (74)...(1129)
26 <400> SEQUENCE: 1
27      aagcttggtta ccgagctcgg atccactagt aacggccgcc agtgtgctgg aattcggctt 60
28      ggggatatcc acc atg gag aca gac aca ctc ctg cta tgg gta ctg ctg 109
29      Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu
30      1 5 10
31      ctc tgg gtt cca ggt tcc act ggt gac tat cca tat gat gtt cca gat 157
32      Leu Trp Val Pro Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp
33      15 20 25
34      tat gct ggg gcc cag ccg gcc aga tct gat atc cag ctg acc cag agc 205
35      Tyr Ala Gly Ala Gln Pro Ala Arg Ser Asp Ile Gln Leu Thr Gln Ser
36      30 35 40
37      cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt 253
38      Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
39      45 50 55 60
40      aag tcc agt caa agt gtt tta tac agt tca aat cag aag aac tac ttg 301
41      Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu
42      65 70 75
43      gcc tgg tac cag cag aag cca ggt aag gct cca aag ctg ctg atc tac 349
44      Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr

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45		80		85		90		
46	tgg gca tcc act agg gaa tct ggt gtg cca agc aga ttc agc ggt agc							397
47	Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser							
48		95		100		105		
49	ggt agc ggt acc gac ttc acc ttc acc atc agc agc ctc cag cca gag							445
50	Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu							
51		110		115		120		
52	gac atc gcc acc tac tac tgc cat caa tac ctc tcc tcg tgg acg ttc							493
53	Asp Ile Ala Thr Tyr Tyr Cys His Gln Tyr Leu Ser Ser Trp Thr Phe							
54		125		130		135		140
55	ggc caa ggg acc aag gtg gaa atc aag agc tct ggc ggt ggc ggc tcc							541
56	Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Gly Gly Gly Gly Ser							
57		145		150		155		
58	gga ggt gga ggc agc gga ggg ggt gga tcc gag gtc caa ctg gtg gag							589
59	Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu							
60		160		165		170		
61	agc ggt gga ggt gtt gtg caa cct ggc cgg tcc ctg cgc ctg tcc tgc							637
62	Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys							
63		175		180		185		
64	tcc tcg tct ggc ttc att ttc agt gac aat tac atg tat tgg gtg aga							685
65	Ser Ser Ser Gly Phe Ile Phe Ser Asp Asn Tyr Met Tyr Trp Val Arg							
66		190		195		200		
67	cag gca cct gga aaa ggt ctt gag tgg gtt gca acc att agt gat ggt							733
68	Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Thr Ile Ser Asp Gly							
69		205		210		215		220
70	ggt agt tac acc tac tat cca gac agt gtg aag gga aga ttt aca ata							781
71	Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile							
72		225		230		235		
73	tcg aga gac aac agc aag aac aca ttg ttc ctg caa atg gac agc ctg							829
74	Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu							
75		240		245		250		
76	aga ccc gaa gac acc ggg gtc tat ttt tgt gca aga ggc tac tat agg							877
77	Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg Gly Tyr Tyr Arg							
78		255		260		265		
79	tac gag ggg gct atg gac tac tgg ggc caa ggg acc ccg gtc acc gtc							925
80	Tyr Glu Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val							
81		270		275		280		
82	tcc tca ccg cgg ctg cag gtc gac gaa caa aaa ctc atc tca gaa gag							973
83	Ser Ser Pro Arg Leu Gln Val Asp Glu Gln Lys Leu Ile Ser Glu Glu							
84		285		290		295		300
85	gat ctg aat gct gtg ggc cag gac acg cag gag gtc atc gtg gtg cca							1021
86	Asp Leu Asn Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro							
87		305		310		315		
88	cac tcc ttg ccc ttt aag gtg gtg gtg atc tca gcc atc ctg gcc ctg							1069
89	His Ser Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu							
90		320		325		330		
91	gtg gtg ctc acc atc atc tcc ctt atc atc ctc atc atg ctt tgg cag							1117
92	Val Val Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln							
93		335		340		345		

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94      aag aag cca cgt tag                                     1132
95      Lys Lys Pro Arg
96      350
98 <210> SEQ ID NO: 2
99 <211> LENGTH: 352
100 <212> TYPE: PRT
101 <213> ORGANISM: Artificial Sequence
102 <220> FEATURE:
103 <223> OTHER INFORMATION: Synthetic construct
104 <400> SEQUENCE: 2
105      Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
106      1          5          10          15
107      Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala
108      20          25          30
109      Gln Pro Ala Arg Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu
110      35          40          45
111      Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln
112      50          55          60
113      Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln
114      65          70          75          80
115      Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr
116      85          90          95
117      Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
118      100         105         110
119      Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr
120      115         120         125
121      Tyr Tyr Cys His Gln Tyr Leu Ser Ser Trp Thr Phe Gly Gln Gly Thr
122      130         135         140
123      Lys Val Glu Ile Lys Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
124      145         150         155         160
125      Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
126      165         170         175
127      Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ser Gly
128      180         185         190
129      Phe Ile Phe Ser Asp Asn Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly
130      195         200         205
131      Lys Gly Leu Glu Trp Val Ala Thr Ile Ser Asp Gly Gly Ser Tyr Thr
132      210         215         220
133      Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
134      225         230         235         240
135      Ser Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp
136      245         250         255
137      Thr Gly Val Tyr Phe Cys Ala Arg Gly Tyr Tyr Arg Tyr Glu Gly Ala
138      260         265         270
139      Met Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Pro Arg
140      275         280         285
141      Leu Gln Val Asp Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala
142      290         295         300
143      Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu Pro

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144      305      310      315      320
145      Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu Thr
146      325      330      335
147      Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg
148      340      345      350
150 <210> SEQ ID NO: 3
151 <211> LENGTH: 1135
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: Synthetic construct
156 <220> FEATURE:
157 <221> NAME/KEY: CDS
158 <222> LOCATION: (74)...(1132)
159 <400> SEQUENCE: 3
160      aagcttggtta ccgagctcgg atccactagt aacggccgcc agtgtgctgg aattcggctt 60
161      ggggatatcc acc atg gag aca gac aca ctc ctg cta tgg gta ctg ctg 109
162      Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu
163      1      5      10
164      ctc tgg gtt cca ggt tcc act ggt gac tat cca tat gat gtt cca gat 157
165      Leu Trp Val Pro Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp
166      15      20      25
167      tat gct ggg gcc cag ccg gcc aga tct gag atc cag ctg cag cag act 205
168      Tyr Ala Gly Ala Gln Pro Ala Arg Ser Glu Ile Gln Leu Gln Gln Thr
169      30      35      40
170      gga cct gag ctg gtg aag cct ggg gct tca gtg aag ata tcc tgc aag 253
171      Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys
172      45      50      55      60
173      gct tct ggt tat tca ttc act gac tac atc ata ttt tgg gtg aag cag 301
174      Ala Ser Gly Tyr Ser Phe Thr Asp Tyr Ile Ile Phe Trp Val Lys Gln
175      65      70      75
176      agc cat gga aag agc ctt gag tgg act gga aat aat aat cct tac tat 349
177      Ser His Gly Lys Ser Leu Glu Trp Thr Gly Asn Asn Asn Pro Tyr Tyr
178      80      85      90
179      ggt agt act agc tac aat ctg aag ttc aag ggc aag gcc aca ttg act 397
180      Gly Ser Thr Ser Tyr Asn Leu Lys Phe Lys Gly Lys Ala Thr Leu Thr
181      95      100      105
182      gta gac aaa tct tcc agc aca gcc tac atg cag ctc aac agt ctg aca 445
183      Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr
184      110      115      120
185      tct gag gac tct gca gtc tat tac tgt gta aga gga gtt tat tac tac 493
186      Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Arg Gly Val Tyr Tyr Tyr
187      125      130      135      140
188      ggt agt agc tac gag gcg ttt cct tac tgg ggc caa ggg act ctg gtc 541
189      Gly Ser Ser Tyr Glu Ala Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val
190      145      150      155
191      act gtc tct gca gga ggt ggc ggc tcc gga gga ggt ggc agc gga ggg 589
192      Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
193      160      165      170

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```

194   ggc gga tcc gat gtt gtg atg acc cag act cca ctc act ttg tgc att   637
195   Gly Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Ile
196           175                               180                               185
197   acc att gga caa cca gcc tcc atc tct tgc aag tca agt cag agc ctc   685
198   Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
199           190                               195                               200
200   tta gat agt gat gga aag aca tat ttg aat tgg ttg tta cag agg cca   733
201   Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
202   205                               210                               215                               220
203   ggc cag tct cca acg cgc cta atc tat ctg gtg tct aaa ctg gac tct   781
204   Gly Gln Ser Pro Thr Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser
205           225                               230                               235
206   gga gtc cct gac agg ttc act ggc agt gga tca ggg aca gat ttc aca   829
207   Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
208           240                               245                               250
209   ctg aaa atc agc aga gtg gag gct gag gat ttg gga att tat tat tgc   877
210   Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
211           255                               260                               265
212   tgg caa ggt gca cat ttt cct cag acg ttc ggt gga ggc acc aag ctg   925
213   Trp Gln Gly Ala His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu
214           270                               275                               280
215   gaa atc aaa ccg cgg ctg cag gtc gac gaa caa aaa ctc atc tca gaa   973
216   Glu Ile Lys Pro Arg Leu Gln Val Asp Glu Gln Lys Leu Ile Ser Glu
217   285                               290                               295                               300
218   gag gat ctg aat gct gtg ggc cag gac acg cag gag gtc atc gtg gtg   1021
219   Glu Asp Leu Asn Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val
220           305                               310                               315
221   cca cac tcc ttg ccc ttt aag gtg gtg gtg atc tca gcc atc ctg gcc   1069
222   Pro His Ser Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala
223           320                               325                               330
224   ctg gtg gtg ctc acc atc atc tcc ctt atc atc ctc atc atg ctt tgg   1117
225   Leu Val Val Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp
226           335                               340                               345
227   cag aag aag cca cgt tag   1135
228   Gln Lys Lys Pro Arg
229           350
231 <210> SEQ ID NO: 4
232 <211> LENGTH: 353
233 <212> TYPE: PRT
234 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Synthetic construct
237 <400> SEQUENCE: 4
238   Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
239           1           5           10           15
240   Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala
241           20           25           30
242   Gln Pro Ala Arg Ser Glu Ile Gln Leu Gln Gln Thr Gly Pro Glu Leu
243           35           40           45

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VERIFICATION SUMMARY

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